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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2010; month=2; day=11; hr=9; min=21; sec=16; ms=677;]

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Application No: 10517225 Version No: 3.0

Input Set:**Output Set:**

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Finished: 2010-02-05 18:23:17.262
Elapsed: 0 hr(s) 0 min(s) 6 sec(s) 940 ms
Total Warnings: 32
Total Errors: 0
No. of SeqIDs Defined: 148
Actual SeqID Count: 148

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Input Set:

Output Set:

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Error code

Error Description

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SEQUENCE LISTING

<110> ALESSI, Dario
 BIONDI, Ricardo
 KOMANDER, David
 VAN, Aalten, Daan

<120> Methods

<130> ERP01.005APC

<140> 10517225

<141> 2010-02-05

<150> PCT/GB2003/002509

<151> 2003-06-09

<150> GB0213186.0

<151> 2002-06-08

<160> 148

<170> PatentIn version 3.1

<210> 1

<211> 4

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (2)..(3)

<223> Any amino acid residue

<400> 1

Phe Xaa Xaa Phe

1

<210> 2

<211> 6

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (2)..(3)

<223> Any amino acid residue

<220>

<221> MISC_FEATURE

<222> (5)..(5)

<223> S or T

<400> 2

Phe Xaa Xaa Phe Xaa Tyr
1 5

<210> 3

<211> 556

<212> PRT

<213> Homo sapiens

<400> 3

Met Ala Arg Thr Thr Ser Gln Leu Tyr Asp Ala Val Pro Ile Gln Ser
1 5 10 15

Ser Val Val Leu Cys Ser Cys Pro Ser Pro Ser Met Val Arg Thr Gln
20 25 30

Thr Glu Ser Ser Thr Pro Pro Gly Ile Pro Gly Gly Ser Arg Gln Gly
35 40 45

Pro Ala Met Asp Gly Thr Ala Ala Glu Pro Arg Pro Gly Ala Gly Ser
50 55 60

Leu Gln His Ala Gln Pro Pro Pro Gln Pro Arg Lys Lys Arg Pro Glu
65 70 75 80

Asp Phe Lys Phe Gly Lys Ile Leu Gly Glu Gly Ser Phe Ser Thr Val
85 90 95

Val Leu Ala Arg Glu Leu Ala Thr Ser Arg Glu Tyr Ala Ile Lys Ile
100 105 110

Leu Glu Lys Arg His Ile Ile Lys Glu Asn Lys Val Pro Tyr Val Thr
115 120 125

Arg Glu Arg Asp Val Met Ser Arg Leu Asp His Pro Phe Phe Val Lys
130 135 140

Leu Tyr Phe Thr Phe Gln Asp Asp Glu Lys Leu Tyr Phe Gly Leu Ser
145 150 155 160

Tyr Ala Lys Asn Gly Glu Leu Leu Lys Tyr Ile Arg Lys Ile Gly Ser

165

170

175

Phe Asp Glu Thr Cys Thr Arg Phe Tyr Thr Ala Glu Ile Val Ser Ala
 180 185 190

Leu Glu Tyr Leu His Gly Lys Gly Ile Ile His Arg Asp Leu Lys Pro
 195 200 205

Glu Asn Ile Leu Leu Asn Glu Asp Met His Ile Gln Ile Thr Asp Phe
 210 215 220

Gly Thr Ala Lys Val Leu Ser Pro Glu Ser Lys Gln Ala Arg Ala Asn
 225 230 235 240

Ser Phe Val Gly Thr Ala Gln Tyr Val Ser Pro Glu Leu Leu Thr Glu
 245 250 255

Lys Ser Ala Cys Lys Ser Ser Asp Leu Trp Ala Leu Gly Cys Ile Ile
 260 265 270

Tyr Gln Leu Val Ala Gly Leu Pro Pro Phe Arg Ala Gly Asn Glu Tyr
 275 280 285

Leu Ile Phe Gln Lys Ile Ile Lys Leu Glu Tyr Asp Phe Pro Glu Lys
 290 295 300

Phe Phe Pro Lys Ala Arg Asp Leu Val Glu Lys Leu Leu Val Leu Asp
 305 310 315 320

Ala Thr Lys Arg Leu Gly Cys Glu Glu Met Glu Gly Tyr Gly Pro Leu
 325 330 335

Lys Ala His Pro Phe Phe Glu Ser Val Thr Trp Glu Asn Leu His Gln
 340 345 350

Gln Thr Pro Pro Lys Leu Thr Ala Tyr Leu Pro Ala Met Ser Glu Asp
 355 360 365

Asp Glu Asp Cys Tyr Gly Asn Tyr Asp Asn Leu Leu Ser Gln Phe Gly
 370 375 380

Cys Met Gln Val Ser Ser Ser Ser Ser Ser His Ser Leu Ser Ala Ser
 385 390 395 400

Asp Thr Gly Leu Pro Gln Arg Ser Gly Ser Asn Ile Glu Gln Tyr Ile
405 410 415

His Asp Leu Asp Ser Asn Ser Phe Glu Leu Asp Leu Gln Phe Ser Glu
420 425 430

Asp Glu Lys Arg Leu Leu Leu Glu Lys Gln Ala Gly Gly Asn Pro Trp
435 440 445

His Gln Phe Val Glu Asn Asn Leu Ile Leu Lys Met Gly Pro Val Asp
450 455 460

Lys Arg Lys Gly Leu Phe Ala Arg Arg Arg Gln Leu Leu Leu Thr Glu
465 470 475 480

Gly Pro His Leu Tyr Tyr Val Asp Pro Val Asn Lys Val Leu Lys Gly
485 490 495

Glu Ile Pro Trp Ser Gln Glu Leu Arg Pro Glu Ala Lys Asn Phe Lys
500 505 510

Thr Phe Phe Val His Thr Pro Asn Arg Thr Tyr Tyr Leu Met Asp Pro
515 520 525

Ser Gly Asn Ala His Lys Trp Cys Arg Lys Ile Gln Glu Val Trp Arg
530 535 540

Gln Arg Tyr Gln Ser His Pro Asp Ala Ala Val Gln
545 550 555

<210> 4
<211> 249
<212> PRT
<213> Homo sapiens

<400> 4

Met Asp Gly Thr Ala Ala Glu Pro Arg Pro Gly Ala Gly Ser Leu Gln
1 5 10 15

His Ala Gln Pro Pro Pro Gln Pro Arg Lys Lys Arg Pro Glu Asp Phe
20 25 30

Lys Phe Gly Lys Ile Leu Gly Glu Gly Ser Phe Ser Thr Val Val Leu
35 40 45

Ala Arg Glu Leu Ala Thr Ser Arg Glu Tyr Ala Ile Lys Ile Leu Glu
50 55 60

Lys Arg His Ile Ile Lys Glu Asn Lys Val Pro Tyr Val Thr Arg Glu
65 70 75 80

Arg Asp Val Met Ser Arg Leu Asp His Pro Phe Phe Val Lys Leu Tyr
85 90 95

Phe Thr Phe Gln Asp Asp Glu Lys Leu Tyr Phe Gly Leu Ser Tyr Ala
100 105 110

Lys Asn Gly Glu Leu Leu Lys Tyr Ile Arg Lys Ile Gly Ser Phe Asp
115 120 125

Glu Thr Cys Thr Arg Phe Tyr Thr Ala Glu Ile Val Ser Ala Leu Glu
130 135 140

Tyr Leu His Gly Lys Gly Ile Ile His Arg Asp Leu Lys Pro Glu Asn
145 150 155 160

Ile Leu Leu Asn Glu Asp Met His Ile Gln Ile Thr Asp Phe Gly Thr
165 170 175

Ala Lys Val Leu Ser Pro Glu Ser Lys Gln Ala Arg Ala Asn Ser Phe
180 185 190

Val Gly Thr Ala Gln Tyr Val Ser Pro Glu Leu Leu Thr Glu Lys Ser
195 200 205

Ala Cys Lys Ser Ser Asp Leu Trp Ala Leu Gly Cys Ile Ile Tyr Gln
210 215 220

Leu Val Ala Gly Leu Pro Pro Phe Arg Ala Gly Asn Glu Tyr Leu Ile
225 230 235 240

Phe Gln Lys Ile Ile Lys Leu Glu Tyr
245

<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Phosphorylation consensus motif

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Any amino acid

<400> 5

Thr Phe Cys Gly Thr Xaa Glu Leu
1 5

<210> 6
<211> 229
<212> PRT
<213> Homo sapiens

<400> 6

Pro Pro Gln Pro Arg Lys Lys Arg Pro Glu Asp Phe Lys Phe Gly Lys
1 5 10 15

Ile Leu Gly Glu Gly Ser Phe Ser Thr Val Val Leu Ala Arg Glu Leu
20 25 30

Ala Thr Ser Arg Glu Tyr Ala Ile Lys Ile Leu Glu Lys Arg His Ile
35 40 45

Ile Lys Glu Asn Lys Val Pro Tyr Val Thr Arg Glu Arg Asp Val Met
50 55 60

Ser Arg Leu Asp His Pro Phe Phe Val Lys Leu Tyr Phe Thr Phe Gln
65 70 75 80

Asp Asp Glu Lys Leu Tyr Phe Gly Leu Ser Tyr Ala Lys Asn Gly Glu
85 90 95

Leu Leu Lys Tyr Ile Arg Lys Ile Gly Ser Phe Asp Glu Thr Cys Thr
100 105 110

Arg Phe Tyr Thr Ala Glu Ile Val Ser Ala Leu Glu Tyr Leu His Gly
115 120 125

Lys Gly Ile Ile His Arg Asp Leu Lys Pro Glu Asn Ile Leu Leu Asn
130 135 140

Glu Asp Met His Ile Gln Ile Thr Asp Phe Gly Thr Ala Lys Val Leu
145 150 155 160

Ser Pro Glu Ser Lys Gln Ala Arg Ala Asn Ser Phe Val Gly Thr Ala
165 170 175

Gln Tyr Val Ser Pro Glu Leu Leu Thr Glu Lys Ser Ala Cys Lys Ser
180 185 190

Ser Asp Leu Trp Ala Leu Gly Cys Ile Ile Tyr Gln Leu Val Ala Gly
195 200 205

Leu Pro Pro Phe Arg Ala Gly Asn Glu Tyr Leu Ile Phe Gln Lys Ile
210 215 220

Ile Lys Leu Glu Tyr
225

<210> 7
<211> 251
<212> PRT
<213> Artificial Sequence

<220>
<223> Modified PDK1

<400> 7

Gly Pro Met Asp Gly Thr Ala Ala Glu Pro Arg Pro Gly Ala Gly Ser
1 5 10 15

Leu Gln His Ala Gln Pro Pro Pro Gln Pro Arg Lys Lys Arg Pro Glu
20 25 30

Asp Phe Lys Phe Gly Lys Ile Leu Gly Glu Gly Ser Phe Ser Thr Val
35 40 45

Val Leu Ala Arg Glu Leu Ala Thr Ser Arg Glu Tyr Ala Ile Lys Ile
50 55 60

Leu Glu Lys Arg His Ile Ile Lys Glu Asn Lys Val Pro Tyr Val Thr
65 70 75 80

Arg Glu Arg Asp Val Met Ser Arg Leu Asp His Pro Phe Phe Val Lys
85 90 95

Leu Tyr Phe Thr Phe Gln Asp Asp Glu Lys Leu Tyr Phe Gly Leu Ser
100 105 110

Tyr Ala Lys Asn Gly Glu Leu Leu Lys Tyr Ile Arg Lys Ile Gly Ser
115 120 125

Phe Asp Glu Thr Cys Thr Arg Phe Tyr Thr Ala Glu Ile Val Ser Ala
130 135 140

Leu Glu Tyr Leu His Gly Lys Gly Ile Ile His Arg Asp Leu Lys Pro
145 150 155 160

Glu Asn Ile Leu Leu Asn Glu Asp Met His Ile Gln Ile Thr Asp Phe
165 170 175

Gly Thr Ala Lys Val Leu Ser Pro Glu Ser Lys Gln Ala Arg Ala Asn
180 185 190

Ser Phe Val Gly Thr Ala Gln Tyr Val Ser Pro Glu Leu Leu Thr Glu
195 200 205

Lys Ser Ala Cys Lys Ser Ser Asp Leu Trp Ala Leu Gly Cys Ile Ile
210 215 220

Tyr Gln Leu Val Ala Gly Leu Pro Pro Phe Arg Ala Gly Asn Glu Tyr
225 230 235 240

Leu Ile Phe Gln Lys Ile Ile Lys Leu Glu Tyr
245 250

<210> 8
<211> 14
<212> PRT
<213> Homo sapiens

<400> 8

Lys Val Pro Tyr Val Thr Arg Glu Arg Asp Val Met Ser Arg
1 5 10

<210> 9
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> PDK1 activity

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> T or S

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Any amino acid residue

<400> 9

Xaa Phe Cys Gly Thr Xaa Glu Leu
1 5

<210> 10
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> PDK2 activity

<220>
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<222> (2)..(3)
<223> Any amino acid residue

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<222> (5)..(5)
<223> S or T

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> P or Y

<400> 10

Pro Xaa Xaa Pro Xaa Xaa
1 5

<210> 11
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Phosphorylated hydrophobic motif

<220>
<221> MISC_FEATURE
<222> (2)..(3)
<223> Any amino acid residue

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Any negatively charged residue

<400> 11

Phe Xaa Xaa Phe Xaa Tyr
1 5

<210> 12
<211> 26
<212> PRT
<213> Homo sapiens

<400> 12

Gln Pro Arg Lys Lys Arg Pro Glu Asp Phe Lys Phe Gly Lys Ile Leu
1 5 10 15

Gly Glu Gly Ser Phe Ser Thr Val Val Leu
20 25

<210> 13
<211> 26
<212> PRT
<213> Homo sapiens

<400> 13

Pro Lys His Arg Val Thr Met Asn Glu Phe Glu Tyr Leu Lys Leu Leu
1 5 10 15

Gly Lys Gly Thr Phe Gly Lys Val Ile Leu
20 25

<210> 14
<211> 26
<212> PRT
<213> Homo sapiens

<400> 14

Gly Pro Glu Lys Ile Arg Pro Glu Cys Phe Glu Leu Leu Arg Val Leu
1 5 10 15

Gly Lys Gly Gly Tyr Gly Lys Val Phe Gln
20 25

<210> 15
<211> 26
<212> PRT
<213> Homo sapiens

<400> 15

Ser Asn Pro His Ala Lys Pro Ser Asp Phe His Phe Leu Lys Val Ile
1 5 10 15

Gly Lys Gly Ser Phe Gly Lys Val Leu Leu
20 25

<210> 16
<211> 26
<212> PRT
<213> Homo sapiens

<400> 16

Gly Ser Glu Lys Ala Asp Pro Ser His Phe Glu Leu Leu Lys Val Leu
1 5 10 15

Gly Gln Gly Ser Phe Gly Lys Val Phe Leu
20 25

<210> 17
<211> 318
<212> PRT
<213> Homo sapiens

<400> 17

Lys Val Phe Gln Val Arg Lys Val Thr Gly Ala Asn Thr Gly Lys Ile
1 5 10 15

Phe Ala Met Lys Val Leu Lys Lys Ala Met Ile Val Arg Asn Ala Lys

20

25

30

Asp Thr Ala His Thr Lys Ala Glu Arg Asn Ile Leu Glu Glu Val Lys
 35 40 45

His Pro Phe Ile Val Asp Leu Ile Tyr Ala Phe Gln Thr Gly Gly Lys
 50 55 60

Leu Tyr Leu Ile Leu Glu Tyr Leu Ser Gly Gly Glu Leu Phe Met Gln
 65 70 75 80

Leu Glu Arg Glu Gly Ile Phe Met Glu Asp Thr Ala Cys Phe Tyr Leu
 85 90 95

Ala Glu Ile Ser Met Ala Leu Gly His Leu His Gln Lys Gly Ile Ile
 100 105 110

Tyr Arg Asp Leu Lys Pro Glu Asn Ile Met Leu Asn His Gln Gly His
 115 120 125

Val Lys Leu Thr Asp Phe Gly Leu Cys Lys Glu Ser Ile His Asp Gly
 130 135 140

Thr Val Thr His Thr Phe Cys Gly Thr Ile Glu Tyr Met Ala Pro Glu
 145 150 155 160

Ile Leu Met Arg Ser Gly His Asn Arg Ala Val Asp Trp Trp Ser Leu
 165 170 175

Gly Ala Leu Met Tyr Asp Met Leu Thr Gly Ala Pro Pro Phe Thr Gly
 180 185 190

Glu Asn Arg Lys Lys Thr Ile Asp Lys Ile Leu Lys Cys Lys Leu Asn
 195 200 205

Leu Pro Pro Tyr Leu Thr Gln Glu Ala Arg Asp Leu Leu Lys Lys Leu
 210 215 220

Leu Lys Arg Asn Ala Ala Ser Arg Leu Gly Ala Gly Pro Gly Asp Ala
 225 230 235 240

Gly Glu Val Gln Ala His Pro Phe Phe Arg His Ile Asn Trp Glu Glu
 245 250 255

Leu Leu Ala Arg Lys Val Glu Pro Pro Phe Lys Pro Leu Leu Gln Ser
260 265 270

Glu Glu Asp Val Ser Gln Phe Asp Ser Lys Phe Thr Arg Gln Thr Pro
275 280 285

Val Asp Ser Pro Asp Asp Ser Thr Leu Ser Glu Ser Ala Asn Gln Val
290 295 300

Phe Leu Gly Phe Thr Tyr Val Ala Pro Ser Val Leu Glu Ser
305 310 315